

**results of BLAST****BLASTP 2.2.6 [Apr-09-2003]****Reference:**

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1051730124-02802-29002

Query=

(10 letters)

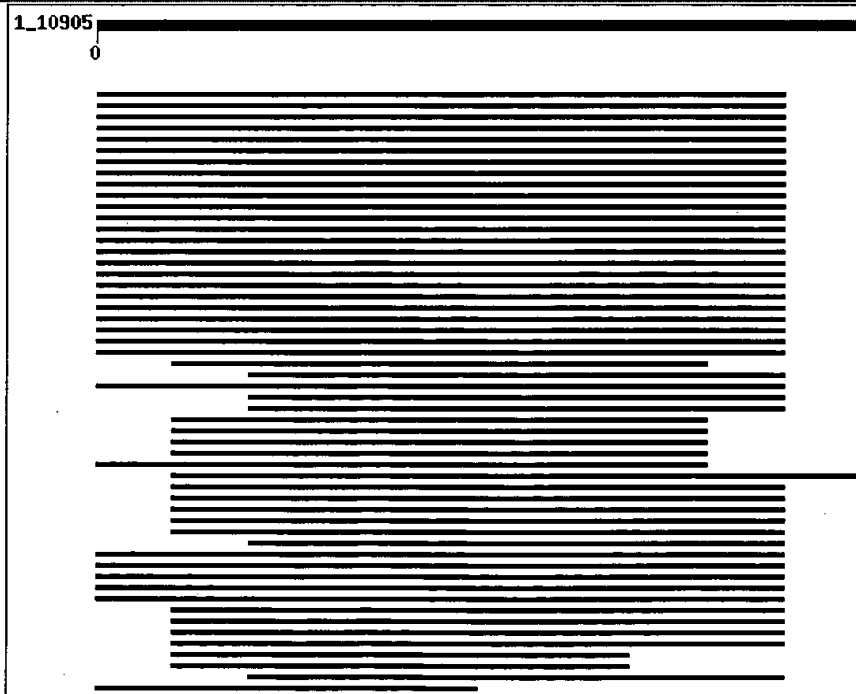
Database: All non-redundant GenBank CDS
translations+PDB+SwissProt+PIR+PRF

1,419,727 sequences; 456,953,620 total letters

If you have any problems or questions with the results of this search
please refer to the [BLAST FAQs](#)

[Taxonomy reports](#)**Distribution of 101 Blast Hits on the Query Sequence**

Mouse-over to show defline and scores. Click to show alignments



Sequences producing significant alignments:

Score	E
(bits)	Value

gi 30048092 gb AAH50279.1	Similar to dynamin 1 [Homo sapiens]	35	0.12	
gi 539581 pir B40671	dynamin, internal form 2, short C-ter...	35	0.12	
gi 4758182 ref NP_004399.1	dynamin 1; dynamin; dynamin1; D...	35	0.12	L
gi 181855 gb AAA02806.1	dynamin	35	0.12	L
gi 487853 gb AAA37319.1	dynamin	35	0.12	L
gi 487855 gb AAA37323.1	dynamin	35	0.12	L
gi 20824027 ref XP_130133.1	dynamin [Mus musculus]	35	0.12	L
gi 539580 pir A40671	dynamin, internal form 1, long C-term...	35	0.12	
gi 18093102 ref NP_542420.1	dynamin 1 [Rattus norvegicus] ...	35	0.12	L
gi 21961254 gb AAH34679.1	Dnm protein [Mus musculus]	35	0.12	
gi 181853 gb AAA02805.1	dynamin	35	0.12	
gi 729381 sp P39053 DYN1 MOUSE	Dynamin-1 (Dynamin BREDNM19)...	35	0.12	L
gi 585074 sp Q08877 DYN3 RAT	Dynamin 3 (Dynamin, testicular...	31	2.3	L
gi 26331226 dbj BAC29343.1	unnamed protein product [Mus mu...	31	2.3	L
gi 24308091 ref NP_056384.1	KIAA0820 protein [Homo sapiens]...	31	2.3	L
gi 28972415 dbj BAC65661.1	mKIAA0820 protein [Mus musculus]	31	2.3	
gi 27805466 sp Q9UQ16 DYN3 HUMAN	Dynamin 3 (Dynamin, testic...	31	2.3	L
gi 1835967 gb AAB46800.1	dynamin III isoform=GTPase homolo...	31	2.3	
gi 19924077 ref NP_612547.1	testicular dynamin [Rattus nor...	31	2.3	L
gi 19353648 gb AAH24584.1	9630020E24Rik protein [Mus muscu...	31	2.3	
gi 27369922 ref NP_766234.1	RIKEN cDNA 9630020E24 [Mus mus...	31	2.3	L
gi 20521666 dbj BAA74843.2	KIAA0820 protein [Homo sapiens]	31	2.3	L
gi 21288051 gb EAA00372.1	agCP9929 [Anopheles gambiae str....	25	139	
gi 17540448 ref NP_501236.1	Predicted CDS, putative nuclea...	25	139	L
gi 22988735 ref ZP_00033796.1	hypothetical protein [Burkho...	25	139	
gi 27378665 ref NP_770194.1	blr3554 [Bradyrhizobium japoni...	25	139	
gi 24474936 emb CAC87573.1	trypanothione synthetase [Trypa...	24	186	
gi 17570421 ref NP_509982.1	Putative plasma membrane membr...	24	186	L
gi 29468074 gb AAO00721.1	trypanothione synthetase [Trypan...	24	186	
gi 24655701 ref NP_523793.2	Focal adhesion kinase-like CG1...	24	250	L
gi 6525023 gb AAF15292.1 AF201701.1	focal adhesion kinase h...	24	250	L
gi 6409130 gb AAF07854.1 AF112116.1	focal adhesion kinase h...	24	250	L
gi 6016830 dbj BAA85188.1	focal adhesion kinase [Drosophil...	24	250	L
gi 21289343 gb EAA01636.1	ebiP7766 [Anopheles gambiae str....	24	335	
gi 7657238 ref NP_055240.1	inversin [Homo sapiens] >gi 392...	24	335	L
gi 28372796 gb AAO18093.1	unknown [Babesia microti]	24	335	
gi 15237241 ref NP_200085.1	hypothetical protein; protein ...	24	335	
gi 3925425 gb AAC79457.1	inversin protein alternative isof...	24	335	L
gi 14574596 gb AAD02131.2	inv candidate homolog [Homo sapi...	24	335	
gi 6912374 ref NP_036317.1	forkhead box E2 [Homo sapiens] ...	24	335	L
gi 21222187 ref NP_627966.1	putative membrane protein [Str...	24	335	
gi 6978771 ref NP_037331.1	dynamin 2 [Rattus norvegicus] >...	23	450	L
gi 27806155 ref NP_776893.1	synaptojanin 1 [Bos taurus] >g...	23	450	L
gi 12836637 dbj BAB23745.1	unnamed protein product [Mus mu...	23	450	L
gi 2702321 gb AAC51921.1	synaptojanin [Homo sapiens]	23	450	L
gi 15609426 ref NP_216805.1	cdh [Mycobacterium tuberculosi...	23	450	
gi 28919283 gb EAA28749.1	predicted protein [Neurospora cr...	23	450	
gi 29732208 ref XP_295554.1	hypothetical protein XP_295554...	23	450	L
gi 10720298 sp O18964 SYJ1 BOVIN	Synaptojanin 1 (Synaptic i...	23	450	
gi 16307381 gb AAH10233.1	Dnm2 protein [Mus musculus]	23	450	L
gi 9625476 ref NP_039710.1	predicted 16.3kd protein [Mycob...	23	450	
gi 6681207 ref NP_031897.1	dynamin 2 [Mus musculus] >gi 48...	23	450	L
gi 20521692 dbj BAA74933.2	KIAA0910 protein [Homo sapiens]	23	450	L
gi 4507335 ref NP_003886.1	synaptojanin 1; inositol 5'-pho...	23	450	L
gi 22002044 sp P39054 DYN2 MOUSE	Dynamin 2 (Dynamin UDNM)	23	450	L
gi 6225895 sp P56722 PTPN BOVIN	Protein-tyrosine phosphatas...	23	450	L
gi 24586224 ref NP_724552.1	CG11112-PB [Drosophila melanog...	23	450	L
gi 1363285 pir A36878	dynamin 2 - rat >gi 404073 gb AAA167...	23	450	L

Pepducin

gi 1083647 pir B53165	dynamin II isoform ba - rat	23	450	
gi 24644378 ref NP_730989.1	pollux CG1093-PB >gi 23170404 ...	23	604	L
gi 29727084 ref XP_298121.1	hypothetical protein XP_298121...	23	604	L
gi 1362003 pir S55889	protein phosphatase 2A B regulatory ...	23	604	
gi 25453269 sp Q9GLG4 SG1	PIG Secretogranin I precursor (Sg...	23	604	
gi 11034601 dbj BAB17125.1	P0463F06.12 [Oryza sativa (japo...	23	604	
gi 19112873 ref NP_596081.1	probable serine threonine-prot...	23	604	
gi 22507080 gb AAM97755.1	hypothetical protein [Oryza sati...	23	604	
gi 21427013 gb AAM53039.1 AF262024.1	PJA1 [Homo sapiens]	23	604	L
gi 23103921 ref ZP_00090393.1	hypothetical protein [Azotob...	23	604	
gi 11290035 pir T48835	lethal(2)denticleless related prote...	23	604	
gi 23103819 ref ZP_00090293.1	hypothetical protein [Azotob...	23	604	
gi 13195576 gb AAK15765.1 AF335251.1	Praja1 isoform c [Mus ...	23	604	L
gi 23471390 ref ZP_00126720.1	hypothetical protein [Pseudo...	23	604	
gi 29841092 gb AAP06105.1	similar to GenBank Accession Num...	23	604	
gi 22968437 gb ZP_00016025.1	hypothetical protein [Rhodosp...	23	604	
gi 26381879 dbj BAC25475.1	unnamed protein product [Mus mu...	23	604	L
gi 18403637 ref NP_564595.1	55 kDa B regulatory subunit of...	23	604	
gi 21356709 ref NP_650112.1	CG6923-PA [Drosophila melanoga...	23	604	L
gi 12837873 dbj BAB23982.1	unnamed protein product [Mus mu...	23	604	L
gi 13195574 gb AAK15764.1 AF335250.1	Praja1 isoform a [Mus ...	23	604	L
gi 21295549 gb EAA07694.1	agCP1713. [Anopheles gambiae str....	23	604	
gi 11283372 pir T48801	hypothetical protein 15E6.90 [impor...	23	604	
gi 9629417 ref NP_044638.1	very large tegument protein [Hu...	23	604	
gi 19113573 ref NP_596781.1	similarity to yeast suppressor...	23	604	
gi 25405491 pir G96555	55 kDa B regulatory subunit of phos...	23	604	
gi 22972926 gb ZP_00019777.1	hypothetical protein [Chlorof...	23	604	
gi 22902385 gb AAH37616.1	Pja1 protein [Mus musculus]	23	604	
gi 7511991 pir T13718	pollux gene protein - fruit fly (Dro...	23	604	L
gi 22507073 gb AAM97748.1	hypothetical protein [Oryza sati...	23	604	
gi 1373163 gb AAB02200.1	pollux	23	604	L
gi 23063477 ref ZP_00088208.1	hypothetical protein [Pseudo...	23	604	
gi 23060056 ref ZP_00084981.1	hypothetical protein [Pseudo...	23	604	
gi 20888961 ref XP_146899.1	similar to circumsporozoite pr...	23	604	L
gi 19112067 ref NP_595275.1	26s protease subunit [Schizosa...	23	604	
gi 7492202 pir T42085	MPT4 protein homolog - fission yeast...	23	604	
gi 5305335 gb AAD41594.1 AF071081.1	proline-rich mucin homo...	23	604	
gi 20838555 ref XP_162177.1	hypothetical protein XP_162177...	23	604	L
gi 24644376 ref NP_730988.1	pollux CG1093-PA >gi 7296688 g...	23	604	
gi 12831443 gb AAK08598.1	unknown [Agrobacterium tumefaciens]	22	810	
gi 29738779 ref XP_295680.1	hypothetical protein XP_295680...	22	810	
gi 22093838 dbj BAC07125.1	hypothetical protein-predicted ...	22	810	

Alignments

Get selected sequences

Select all

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☐ >gi|30048092|gb|AAH50279.1| Similar to dynamin 1 [Homo sapiens]
Length = 881

Score = 35.0 bits (75), Expect = 0.12

Identities = 10/10 (100%), Positives = 10/10 (100%)

Query: 1 QVPSRPNRAP 10

QVPSRPNRAP

Sbjct: 861 QVPSRPNRAP 870

☐ >gi|539581|pir|B40671 dynamin, internal form 2, short C-terminal form - human
Length = 851

Score = 35.0 bits (75), Expect = 0.12
Identities = 10/10 (100%), Positives = 10/10 (100%)

Query: 1 QVPSRPNRAP 10
QVPSRPNRAP
Sbjct: 831 QVPSRPNRAP 840

☐ >gi|4758182|ref|NP_004399.1| dynamin 1; dynamin; dynamin1; Dynamin-1 [Homo sapi
gi|461976|sp|Q05193|DYN1 HUMAN Dynamin-1
gi|181849|gb|AAA02803.1| dynamin
Length = 864

Score = 35.0 bits (75), Expect = 0.12
Identities = 10/10 (100%), Positives = 10/10 (100%)

Query: 1 QVPSRPNRAP 10
QVPSRPNRAP
Sbjct: 831 QVPSRPNRAP 840

☐ >gi|181855|gb|AAA02806.1| dynamin
Length = 126

Score = 35.0 bits (75), Expect = 0.12
Identities = 10/10 (100%), Positives = 10/10 (100%)

Query: 1 QVPSRPNRAP 10
QVPSRPNRAP
Sbjct: 106 QVPSRPNRAP 115

☐ >gi|487853|gb|AAA37319.1| dynamin
Length = 243

Score = 35.0 bits (75), Expect = 0.12
Identities = 10/10 (100%), Positives = 10/10 (100%)

Query: 1 QVPSRPNRAP 10
QVPSRPNRAP
Sbjct: 210 QVPSRPNRAP 219

☐ >gi|487855|gb|AAA37323.1| dynamin
Length = 612

Score = 35.0 bits (75), Expect = 0.12
Identities = 10/10 (100%), Positives = 10/10 (100%)

Query: 1 QVPSRPNRAP 10
QVPSRPNRAP
Sbjct: 592 QVPSRPNRAP 601

☐ >gi|20824027|ref|XP_130133.1| dynamin [Mus musculus]
Length = 864

Score = 35.0 bits (75), Expect = 0.12
Identities = 10/10 (100%), Positives = 10/10 (100%)

Query: 1 QVPSRPNRAP 10
QVPSRPNRAP
Sbjct: 827 QVPSRPNRAP 836

☐ >gi|539580|pir||A40671 dynamin, internal form 1, long C-terminal form - human
Length = 864

Score = 35.0 bits (75), Expect = 0.12

Identities = 10/10 (100%), Positives = 10/10 (100%)

Query: 1 QVPSRPNRAP 10
QVPSRPNRAP
Sbjct: 831 QVPSRPNRAP 840

☐ >gi|18093102|ref|NP_542420.1| dynamin 1 [Rattus norvegicus]
gi|118966|sp|P21575|DYN1_RAT Dynamamin-1 (D100) (Dynamamin, brain) (B-dynamamin)
gi|111573|pir|S11508 D100 protein - rat
gi|56054|emb|CAA38397.1| D100 [Rattus norvegicus]
gi|227123|prf|1614348A dynamin 1 D100 protein
Length = 851

Score = 35.0 bits (75), Expect = 0.12
Identities = 10/10 (100%), Positives = 10/10 (100%)

Query: 1 QVPSRPNRAP 10
QVPSRPNRAP
Sbjct: 831 QVPSRPNRAP 840

☐ >gi|21961254|gb|AAH34679.1| Dnm protein [Mus musculus]
Length = 867

Score = 35.0 bits (75), Expect = 0.12
Identities = 10/10 (100%), Positives = 10/10 (100%)

Query: 1 QVPSRPNRAP 10
QVPSRPNRAP
Sbjct: 831 QVPSRPNRAP 840

☐ >gi|181853|gb|AAA02805.1| dynamin
Length = 131

Score = 35.0 bits (75), Expect = 0.12
Identities = 10/10 (100%), Positives = 10/10 (100%)

Query: 1 QVPSRPNRAP 10
QVPSRPNRAP
Sbjct: 106 QVPSRPNRAP 115

☐ >gi|729381|sp|P39053|DYN1_MOUSE Dynamamin-1 (Dynamamin BREDNM19)
gi|487857|gb|AAA37324.1| dynamin
Length = 861

Score = 35.0 bits (75), Expect = 0.12
Identities = 10/10 (100%), Positives = 10/10 (100%)

Query: 1 QVPSRPNRAP 10
QVPSRPNRAP
Sbjct: 827 QVPSRPNRAP 836

☐ >gi|585074|sp|Q08877|DYN3_RAT Dynamamin 3 (Dynamamin, testicular) (T-dynamamin)
gi|2143992|pir|I55498 testicular dynamamin - rat
gi|391872|dbj|BAA03161.1| testicular dynamamin [Rattus norvegicus]
Length = 848

Score = 30.8 bits (65), Expect = 2.3
Identities = 9/10 (90%), Positives = 9/10 (90%)

Query: 1 QVPSRPNRAP 10
QVPSRP RAP
Sbjct: 823 QVPSRPTRAP 832

☐ >gi|26331226|dbj|BAC29343.1| unnamed protein product [Mus musculus]
Length = 863

Score = 30.8 bits (65), Expect = 2.3
Identities = 9/10 (90%), Positives = 9/10 (90%)

Query: 1 QVPSRPNRAP 10
QVPSRP RAP
Sbjct: 827 QVPSRPTRAP 836

☐ >gi|24308091|ref|NP_056384.1| KIAA0820 protein [Homo sapiens]
gi|12052944|emb|CAB66647.1| hypothetical protein [Homo sapiens]
Length = 863

Score = 30.8 bits (65), Expect = 2.3
Identities = 9/10 (90%), Positives = 9/10 (90%)

Query: 1 QVPSRPNRAP 10
QVPSRP RAP
Sbjct: 827 QVPSRPTRAP 836

☐ >gi|28972415|dbj|BAC65661.1| mKIAA0820 protein [Mus musculus]
Length = 452

Score = 30.8 bits (65), Expect = 2.3
Identities = 9/10 (90%), Positives = 9/10 (90%)

Query: 1 QVPSRPNRAP 10
QVPSRP RAP
Sbjct: 416 QVPSRPTRAP 425

☐ >gi|27805466|sp|Q9UQ16|DYN3 HUMAN Dynamin 3 (Dynamin, testicular) (T-dynamin)
Length = 859

Score = 30.8 bits (65), Expect = 2.3
Identities = 9/10 (90%), Positives = 9/10 (90%)

Query: 1 QVPSRPNRAP 10
QVPSRP RAP
Sbjct: 823 QVPSRPTRAP 832

☐ >gi|1835967|gb|AAB46800.1| dynamin III isoform=GTPase homolog {C-terminal, alter
spliced} [rats, Sprague-Dawley, brain, Peptide Partial,
42 aa]
Length = 42

Score = 30.8 bits (65), Expect = 2.3
Identities = 9/10 (90%), Positives = 9/10 (90%)

Query: 1 QVPSRPNRAP 10
QVPSRP RAP
Sbjct: 6 QVPSRPTRAP 15

☐ >gi|19924077|ref|NP_612547.1| testicular dynamin [Rattus norvegicus]
gi|6409115|gb|AAF07848.1|AF201839.1 dynamin IIIb isoform [Rattus norvegicus]
Length = 869

Score = 30.8 bits (65), Expect = 2.3
Identities = 9/10 (90%), Positives = 9/10 (90%)

Query: 1 QVPSRPNRAP 10
QVPSRP RAP
Sbjct: 833 QVPSRPTRAP 842

☐ >gi|19353648|gb|AAH24584.1| 9630020E24Rik protein [Mus musculus]
Length = 319

Score = 30.8 bits (65), Expect = 2.3
Identities = 9/10 (90%), Positives = 9/10 (90%)

Query: 1 QVPSRPNRAP 10
QVPSRP RAP
Sbjct: 294 QVPSRPTRAP 303

☐ >gi|27369922|ref|NP_766234.1| RIKEN cDNA 9630020E24 [Mus musculus]
gi|26340464|dbj|BAC33895.1| unnamed protein product [Mus musculus]
Length = 859

Score = 30.8 bits (65), Expect = 2.3
Identities = 9/10 (90%), Positives = 9/10 (90%)

Query: 1 QVPSRPNRAP 10
QVPSRP RAP
Sbjct: 823 QVPSRPTRAP 832

☐ >gi|20521666|dbj|BAA74843.2| KIAA0820 protein [Homo sapiens]
Length = 892

Score = 30.8 bits (65), Expect = 2.3
Identities = 9/10 (90%), Positives = 9/10 (90%)

Query: 1 QVPSRPNRAP 10
QVPSRP RAP
Sbjct: 856 QVPSRPTRAP 865

☐ >gi|21288051|gb|EAA00372.1|. agCP9929 [Anopheles gambiae str. PEST]
Length = 332

Score = 24.8 bits (51), Expect = 139
Identities = 8/13 (61%), Positives = 10/13 (76%), Gaps = 3/13 (23%)

Query: 1 QVPSRP---NRAP 10
QVP+RP +RAP
Sbjct: 180 QVPNRAPVDRAP 192

☐ >gi|17540448|ref|NP_501236.1| Predicted CDS, putative nuclear protein family me
specific [Caenorhabditis elegans]
gi|7503465|pir|T25752 hypothetical protein F45E4.4 - Caenorhabditis elegans
gi|13559603|gb|AAK29815.1| Hypothetical protein F45E4.4 [Caenorhabditis elegans]
Length = 2361

Score = 24.8 bits (51), Expect = 139
Identities = 8/11 (72%), Positives = 10/11 (90%), Gaps = 1/11 (9%)

Query: 1 QVPSR-PNRAP 10
QVPSR P+R+P
Sbjct: 1405 QVPSRQPSRSP 1415

☐ >gi|22988735|ref|ZP_00033796.1| hypothetical protein [Burkholderia fungorum]
Length = 412

Score = 24.8 bits (51), Expect = 139
Identities = 7/8 (87%), Positives = 8/8 (100%)

Query: 2 VPSRPNRA 9
VPSRP+RA

Sbjct: 111 VPSRPSRA 118

☐ >gi|27378665|ref|NP_770194.1| blr3554 [Bradyrhizobium japonicum]
 gi|27351814|dbj|BAC48819.1| blr3554 [Bradyrhizobium japonicum USDA 110]
 Length = 136

Score = 24.8 bits (51), Expect = 139
 Identities = 7/8 (87%), Positives = 7/8 (87%)

Query: 3 PSRPNRAP 10

PSRPNR P

Sbjct: 43 PSRPNRDP 50

☐ >gi|24474936|emb|CAC87573.1| trypanothione synthetase [Trypanosoma brucei]
 Length = 627

Score = 24.4 bits (50), Expect = 186
 Identities = 7/8 (87%), Positives = 7/8 (87%)

Query: 3 PSRPNRAP 10

PSRPNR P

Sbjct: 189 PSRPNRNP 196

☐ >gi|17570421|ref|NP_509982.1| Putative plasma membrane protein, with a
 transmembrane domains, nematode specific [Caenorhabditis
 elegans]
 gi|7510333|pir|T27257 hypothetical protein Y62H9A.1 - Caenorhabditis elegans
 gi|3881218|emb|CAA21558.1| Hypothetical protein Y62H9A.1 [Caenorhabditis elegans]
 Length = 366

Score = 24.4 bits (50), Expect = 186
 Identities = 8/11 (72%), Positives = 8/11 (72%), Gaps = 1/11 (9%)

Query: 1 QVPSRP-NRAP 10

VPSRP NR P

Sbjct: 349 HVPSRPTNRVP 359

☐ >gi|29468074|gb|AA000721.1| trypanothione synthetase [Trypanosoma brucei brucei]
 Length = 627

Score = 24.4 bits (50), Expect = 186
 Identities = 7/8 (87%), Positives = 7/8 (87%)

Query: 3 PSRPNRAP 10

PSRPNR P

Sbjct: 189 PSRPNRNP 196

☐ >gi|24655701|ref|NP_523793.2| Focal adhesion kinase-like CG10023-PA
 gi|24655706|ref|NP_725891.1| Focal adhesion kinase-like CG10023-PB
 gi|24655711|ref|NP_725892.1| Focal adhesion kinase-like CG10023-PC
 gi|7302478|gb|AAF57562.1| CG10023-PA [Drosophila melanogaster]
 gi|21645172|gb|AAM70852.1| CG10023-PB [Drosophila melanogaster]
 gi|21645173|gb|AAM70853.1| CG10023-PC [Drosophila melanogaster]
 Length = 1200

Score = 24.0 bits (49), Expect = 250
 Identities = 8/9 (88%), Positives = 8/9 (88%), Gaps = 1/9 (11%)

Query: 2 VPSR-PNRA 9

VPSR PNRA

Sbjct: 943 VPSRPPNRA 951

☐ >gi|6525023|gb|AAF15292.1|AF201701.1 focal adhesion kinase homolog FAK56 [Droso

Length = 1200

Score = 24.0 bits (49), Expect = 250
Identities = 8/9 (88%), Positives = 8/9 (88%), Gaps = 1/9 (11%)

Query: 2 VPSR-PNRA 9
VPSR PNRA
Sbjct: 943 VPSRPPNRA 951

☐ >gi|6409130|gb|AAF07854.1|AF112116.1 focal adhesion kinase homolog DFak56 [Dros]
Length = 1200

Score = 24.0 bits (49), Expect = 250
Identities = 8/9 (88%), Positives = 8/9 (88%), Gaps = 1/9 (11%)

Query: 2 VPSR-PNRA 9
VPSR PNRA
Sbjct: 943 VPSRPPNRA 951

☐ >gi|6016830|dbj|BAA85188.1| focal adhesion kinase [Drosophila melanogaster]
Length = 1198

Score = 24.0 bits (49), Expect = 250
Identities = 8/9 (88%), Positives = 8/9 (88%), Gaps = 1/9 (11%)

Query: 2 VPSR-PNRA 9
VPSR PNRA
Sbjct: 941 VPSRPPNRA 949

☐ >gi|21289343|gb|EAA01636.1| ebiP7766 [Anopheles gambiae str. PEST]
Length = 459

Score = 23.5 bits (48), Expect = 335
Identities = 9/19 (47%), Positives = 9/19 (47%), Gaps = 10/19 (52%)

Query: 2 VPSRPN-----RAP 10
VPSRPN RAP
Sbjct: 208 VPSRPNSSGGRTTDASRAP 226

☐ >gi|7657238|ref|NP_055240.1| inversin [Homo sapiens]
gi|3925387|gb|AAC79436.1| inversin protein [Homo sapiens]
gi|3925424|gb|AAC79456.1| inversin protein [Homo sapiens]
Length = 1065

Score = 23.5 bits (48), Expect = 335
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 2 VPSRPNRAP 10
VPSR +RAP
Sbjct: 632 VPSRQSRAP 640

☐ >gi|28372796|gb|AAO18093.1| unknown [Babesia microti]
Length = 253

Score = 23.5 bits (48), Expect = 335
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 2 VPSRPNRAP 10
VPSR+ AP
Sbjct: 88 VPSRPHSAP 96

☐ >gi|15237241|ref|NP_200085.1| hypothetical protein; protein id: At5g52730.1 [Ara thaliana]

gi|8953728|dbj|BAA98091.1| emb|CAA71173.1-gene_id:F6N7.22-similar to unknown prot
[Arabidopsis thaliana]
Length = 185

Score = 23.5 bits (48), Expect = 335
Identities = 8/11 (72%), Positives = 8/11 (72%), Gaps = 3/11 (27%)

Query: 3 PSR---PNRAP 10
PSR PNRAP
Sbjct: 140 PSREPEPNRAP 150

☐ >gi|3925425|gb|AAC79457.1| inversin protein alternative isoform [Homo sapiens]
Length = 895

Score = 23.5 bits (48), Expect = 335
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 2 VPSRPNRAP 10
VPSR +RAP
Sbjct: 632 VPSRQSRAP 640

☐ >gi|14574596|gb|AAD02131.2| inv candidate homolog [Homo sapiens]
Length = 1013

Score = 23.5 bits (48), Expect = 335
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 2 VPSRPNRAP 10
VPSR +RAP
Sbjct: 580 VPSRQSRAP 588

☐ >gi|6912374|ref|NP_036317.1| forkhead box E2 [Homo sapiens]
gi|20177899|sp|Q99526|FXE2 HUMAN Forkhead box protein E2 (HNF-3/fork head-like p
(HFKH4)
gi|1770432|emb|CAA64246.1| fork head like protein [Homo sapiens]
Length = 500

Score = 23.5 bits (48), Expect = 335
Identities = 8/11 (72%), Positives = 8/11 (72%), Gaps = 2/11 (18%)

Query: 2 VPSR--PNRAP 10
VP R PNRAP
Sbjct: 323 VPPRAPPNRAP 333

☐ >gi|21222187|ref|NP_627966.1| putative membrane protein [Streptomyces coelicolor
gi|10432480|emb|CAC10314.1| putative membrane protein [Streptomyces coelicolor A3
Length = 180

Score = 23.5 bits (48), Expect = 335
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 QVPSRPNRA 9
Q P+RPNRA
Sbjct: 6 QPPARPNRA 14

☐ >gi|6978771|ref|NP_037331.1| dynamin 2 [Rattus norvegicus]
gi|729380|sp|P39052|DYN2 RAT Dynamin 2
gi|1083646|pir|A53165 dynamin II isoform aa - rat
gi|416396|gb|AAA19736.1| dynamin IIaa
Length = 870

Score = 23.1 bits (47), Expect = 450
Identities = 7/10 (70%), Positives = 8/10 (80%)

chimera (kī-mēr'ă, kī-)

1. In experimental embryology, the individual produced by grafting an embryonic part of one animal on to the embryo of another, either of the same or of another species.
2. An organism that has received a transplant of genetically and immunologically different tissue, such as bone marrow.
3. Dizygotic twins that retain each other as immunologically distinct types of erythrocytes.
4. A protein fusion in which two different proteins are linked via peptide bonds; usually genetically engineered. Chimeric antibodies may have the Fab fragment from one species fused with the Fc fragment from another.
5. Any macromolecule fusion formed by two or more macromolecules from different species or from different genes.

[L. *Chimaera*, G. *Chimaira*, mythic monster (lit. a she-goat)]

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☐ 1: Biol Chem 2003 Feb;384(2):193-202

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Wang H, Reiser G.

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Institut für Neurobiochemie, Medizinische Fakultät der
Otto-von-Guericke-Universität Magdeburg, Leipziger Strasse 44, D-39120
Magdeburg, Germany.

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Resources

Signaling by the protease thrombin has started to be appreciated in cell biology, especially since the gene for protease-activated receptor-1 (PAR-1) has been cloned. Apart from the central role of thrombin in blood coagulation and wound healing, thrombin also regulates cellular functions in a large variety of cells through PAR-1, PAR-3 and PAR-4. Receptors are activated by a proteolytic cleavage mechanism via G protein-coupled signaling pathways. Accumulating evidence shows that thrombin changes the morphology of neurons and astrocytes, induces glial cell proliferation, and even exerts, depending on the concentration applied, either cytoprotective or cytotoxic effects on neural cells. These effects may be mediated, through either distinct or overlapping signal transduction cascades, by activation of PARs. This review focuses on the underlying signaling events initiated by thrombin in neuronal and glial cells, to summarize our understanding of the intracellular signaling machinery linking thrombin receptors to their potential physiological and pathological functions in the CNS.

PMID: 12675511 [PubMed - in process]

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